## THAT WHICH IS CLAIMED:

- 1. An isolated nucleic acid molecule having a nucleotide sequence encoding a Bt toxin receptor, said sequence selected from the group consisting of:
- a) a nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5;
- b) a nucleotide sequence having at least about 60 % identity to the nucleotide sequence of a);
- c) a nucleotide sequence having at least about 70 % identity to the nucleotide sequence of a);
- d) a nucleotide sequence having at least about 75 % identity to the nucleotide sequence of a);
- e) a nucleotide sequence having at least about 85 % identity to the nucleotide sequence of a);
- f) a nucleotide sequence having at least about 95 % identity to the nucleotide sequence of a);
- g) a nucleotide sequence consisting of at least 22 contiguous nucleotides of the nucleotide sequence set forth in SEQ ID NO:1;
- h) a nucleotide sequence consisting of at least about 15 contiguous nucleotides of the nucleotide sequence set forth in SEQ ID NO:3, or SEQ ID NO:5;
- i) a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence of a); and
  - 2. The nucleic acid molecule of claim 1, wherein said toxin is a Cry1A toxin.
- 3. The nucleic acid of claim 2, wherein said Cry1A toxin is a Cry1A(b) toxin.
- 4. An isolated polypeptide having the amino acid sequence selected from the group consisting of:
- a) an amino acid sequence set forth in SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6;

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- an amino acid sequence having at least about 52% identity to the b) amino acid sequence set forth in SEQ ID NO: 2;
- an amind acid sequence having at least about 60 % identity to the amino acid sequence of a);
- an amino adid sequence having at least about 70 % identity to the amino acid sequence of a);
- e) an amino acid sequence having at least about 75 % identity to an amino acid sequence of a);
- f) an amino acid sequence having at least about 85 % identity to an amino acid sequence of a);
- g) an amino acid sequence having at least about 95 % identity to an amino acid sequence of a);
- h) an amino acid combrising at least about 15 contiguous residues of the amino acid nucleotide sequence of a);
- i) an amino acid sequence encoded by a nucleotide sequence according to claim 1;
  - j) a variant of the amind acid sequence of a);
  - k) a fragment of the amino acid sequence of a); and
  - 1) a fragment of the amino acid sequence of a) that binds Bt toxin.
- 5. A fusion polypeptide comprising the polypeptide of claim 4, and at least one polypeptide of interest.
- 6. The fusion polypeptide of claim 5, wherein said polypeptide of interest is a toxin receptor.
- An expression cassette comprising a nucleotide sequence encoding the 7. fusion polypeptide of claim 5, wherein said nucleotide sequence is operably linked to a promoter that drives expression in a cell of interest.
  - The expression cassette of claim 7/wherein said polypeptide of interest is a 8.

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toxin receptor.

- 9. An antibody preparation specific for the polypeptide of claim 4.
- 10. An expression cassette comprising at least one nucleotide sequence according to claim 1, wherein said nucleotide sequence is operably linked to a promoter that drives expression in a cell of interest.

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- 11. The expression cassette of claim 10, wherein said cell of interest is an insect or mammalian cell.
- 12. The expression cassette of claim 10 wherein said cell of interest is a microorganism.

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13. The expression cassette of claim 12 wherein said microorganism is yeast or bacteria.

14. A vector for delivery of a nucleotide sequence to a cell of interest, the vector comprising at least one nucleotide sequence according to claim 1.

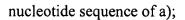
15. A cell containing/the vector of claim 14.

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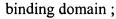
16. A transformed cell of interest having stably incorporated within its genome a nucleotide sequence selected from the group consisting of:

- a) a nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5;
- b) a nucleotide sequence having at least about 60 % identity to the nucleotide sequence of a);
- c) a nucleotide sequence having at least about 70 % identity to the nucleotide sequence of a);
  - d) a nucleotide sequence having at least about 75 % identity to the

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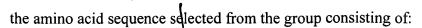
- e) a nucleotide sequence having at least about 85 % identity to the nucleotide sequence of a);
- f) a nucleotide sequence having at least about 95 % identity to the nucleotide sequence of a);
- g) a nucleotide sequence consisting of at least 22 contiguous nucleotides of the nucleotide sequence set forth in SEQ ID NO:1;
- h) a nucleotide sequence consisting of at least about 15 contiguous nucleotides of the nucleotide sequence set forth in SEQ ID NO:3, or SEQ ID NO:5;
- i) a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence of a); and
  - 17. The transformed cell of claim 16, wherein said cell is a plant cell.
- 18. The transformed cell of claim 17, wherein said plant cell is monocotyledonous.
- 19. A method for screening for ligands that bind *Bt* toxin receptor, said method comprising:
- i) providing at least one Bt toxin receptor polypeptide according to claim 4;
- ii) contacting said polypeptide with a sample and a control ligand under conditions promoting binding and
- iii) determining binding characteristics of said sample ligand, relative to said control ligand.
- 20. A method for screening for ligands that bind *Bt* toxin receptor, said method comprising:
- i) providing at least one B toxin receptor polypeptide having the amino acid sequence selected from the group consisting of a, b, c, d, e, f, g, h, i, and j of claim 4 in cells expressing said polypeptide wherein said polypeptide comprises a toxin



- ii) \ contacting said cells with a sample and a control ligand under conditions promoting binding; and
- iii) determining binding characteristics of said sample ligand, relative to said control ligand.
  - 21. The method of claim 20 wherein said toxin is a Cry1A toxin.
- 22. A method for screening for toxins that bind Bt toxin receptor, said method comprising the steps of claim 20 further comprising determining viability of said cells contacted with a sample ligand relative to said cells contacted with a control ligand.
- 23. The method of claim 20, wherein said sample ligand is a chimeric polypeptide comprising at least one primary polypeptide that binds a polypeptide having the amino acid sequence selected from the group consisting of:
- a) an amino acid sequence set forth in SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6;
- b) an amino acid sequence having at least about 52% identity to the amino acid sequence set forth in SEQ ID NO: 2;
- c) an amino acid sequence having at least about 60 % identity to the amino acid sequence of a);
- d) an amino acid sequence having at least about 70 % identity to the amino acid sequence of a);
- e) an amino acid sequence having at least about 75 % identity to an amino acid sequence of a);
- f) an amino acid sequence having at least about 85 % identity to an amino acid sequence of a);
- g) an amino acid sequence having at least about 95 % identity to an amino acid sequence of a);
- h) an amino acid comprising at least about 15 contiguous residues of the amino acid nucleotide sequence of a);



- i) an amino acid sequence encoded by a nucleotide sequence having at least about 60 % identity to the nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 3; and
  - j) a variant of the amino acid sequence of a).
- 24. The method of claims 21, wherein said sample ligand is a chimeric polypeptide comprising at least one primary polypeptide that binds a polypeptide having the amino acid sequence selected from the group consisting of:
- a) an amino acid/sequence set forth in SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6;
- b) an amino acid sequence having at least about 52% identity to the amino acid sequence set forth in SEQID NO: 2;
- c) an amino acid sequence having at least about 60 % identity to the amino acid sequence of a);
- d) an amino acid sequence traving at least about 70 % identity to the amino acid sequence of a);
- e) an amino acid sequence having at least about 75 % identity to an amino acid sequence of a);
- f) an amino acid sequence having at least about 85 % identity to an amino acid sequence of a);
- g) an amino acid sequence having at least about 95 % identity to an amino acid sequence of a);
- h) an amino acid comprising at least about 15 contiguous residues of the amino acid nucleotide sequence of a);
- i) an amino acid sequence encoded by a nucleotide sequence having at least about 60 % identity to the nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5; and
  - j) a variant of the amino acid sequence of a).
- 25. The method of claims 22, wherein said sample light is a chimeric polypeptide comprising at least one primary polypeptide that binds a polypeptide having



- a) an amino acid sequence set forth in SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6;
- b) an amino acid sequence having at least about 52% identity to the amino acid sequence set forth in SEQ ID NO: 2;
- c) an amino acid sequence having at least about 60 % identity to the amino acid sequence of a);
- d) an amino acid sequence having at least about 70 % identity to the amino acid sequence of a);
- e) an amino acid sequence having at least about 75 % identity to an amino acid sequence of a);
- f) an amino acid sequence having at least about 85 % identity to an amino acid sequence of a);
- g) an amino acid sequence having at least about 95 % identity to an amino acid sequence of a);
- h) an amino acid comprising at least about 15 contiguous residues of the amino acid nucleotide sequence of a);
- i) an amino acid sequence encoded by a nucleotide sequence having at least about 60 % identity to the nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5; and
  - j) a variant of the amino acid sequence of a).

